Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Original) A method of identifying an exon in a eukaryotic genomic fragment, the method comprising:

expressing a population of subsequences of the genomic fragment in a phage display library, wherein the population comprises protein-encoding subsequences and noncoding subsequences;

screening the phage display library with a binding partner to identify an expressed subsequence that specifically binds to the binding partner; and

mapping the expressed subsequence to the physical location in the genomic fragment, thereby identifying the exon.

2. (Original) The method of claim 1, wherein the binding partner is an antibody, an enzyme or a receptor.

3. (Original) The method of claim 2, wherein the binding partner is an antibody.

4. (Original) The method of claim 3, wherein the antibody is a single chain antibody.

5. (Original) The method of claim 1, wherein the binding partner is expressed by a phage display library.

6. (Original) The method of claim 5, wherein the phage display library is an antibody phage display library generated using mRNA isolated from a stimulated B cell or a naïve B cell.

7. (Original) The method of claim 6, wherein mRNA isolated from the stimulated B cell is mRNA isolated from a stimulated splenic B cell that is isolated from an animal immunized with a composition comprising the protein epitope encoded by the genomic sequence or a nucleic acid encoding the protein epitope.

8. (Original) The method of claim 1, wherein the expressed subsequences are from about 100 base pairs to about 300 base pairs in length.

9. (Original) The method of claim 1, wherein the genomic fragment is from a mammalian genome.

10. (Original) The method of claim 1, further wherein the exon is abnormally expressed in a cell of an individual with a disease or condition.

11. (Original) The method of claim 10, wherein the cell has a genomic translocation involving the exon sequence.

12. (Original) The method of claim 10, wherein the disease is cancer.

13. (Original) The method of claim 1, further comprising a step of enriching for phage expressing subsequences of the genomic fragment that are exons.

14. (Original) The method of claim 13, wherein the step of enriching comprises incubating the phage library with a binding partner specific for a peptide encoded by a subsequence that does not encode a peptide in vivo, and removing phage expressing the peptide from the library.

15. (Original) The method of claim 14, wherein the subsequence that does not encode a peptide in vivo is a repetitive sequence.

16. (Original) The method of claim 15, wherein the repetitive sequence is an Alu sequence or a Kpn sequence.

17-28. (Canceled)